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0 2002

RECEIVED

RAW SEQUENCE LISTING

DATE: 08/13/2002

PATENT APPLICATION: US/09/762,097A

TIME: 13:31:17

Input Set : A:\Seq LIST.txt

Output Set: N:\CRF3\08132002\I762097A.raw

ENTERED

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3 <110> APPLICANT: HERSHFIELD, MICHAEL S.
4   KELLY, SUSAN J.
6 <120> TITLE OF INVENTION: URATE OXIDASE
8 <130> FILE REFERENCE: 1579-379
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/762,097A
C--> 11 <141> CURRENT FILING DATE: 2001-08-23
13 <160> NUMBER OF SEQ ID NOS: 13
15 <170> SOFTWARE: PatentIn Ver. 2.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 915
19 <212> TYPE: DNA
20 <213> ORGANISM: Artificial Sequence
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23 <221> NAME/KEY: CDS
24 <222> LOCATION: (1)..(915)
26 <220> FEATURE:
27 <223> OTHER INFORMATION: Description of Artificial Sequence:PBC CHIMERA
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34 gtc cga act ggc tat ggg aag gat atg ata aaa gtt ctc cat att cag   96
35 Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln
36   20               25               30
38 cga gat gga aaa tat cac agc att aaa gag gtg gca act tca gtg caa   144
39 Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
40   35               40               45
42 ctg act ttg agc tcc aaa aaa gat tac ctg cat gga gac aat tca gat   192
43 Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
44   50               55               60
46 gtc atc cct aca gac acc atc aag aac aca gtt aat gtc ctg gcg aag   240
47 Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys
48   65               70               75               80
50 ttc aaa ggc atc aaa agc ata gaa act ttt gct gtg act atc tgt gag   288
51 Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu
52   85               90               95
54 cat ttc ctt tct tcc ttc aag cat gtc atc aga gct caa gtc tat gtg   336
55 His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val
56   100              105              110
58 gaa gaa gtt cct tgg aag cgt ttt gaa aag aat gga gtt aag cat gtc   384
59 Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val
60   115              120              125
62 cat gca ttt att tat act cct act gga acg cac ttc tgt gag gtt gaa   432

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63 His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
64      130      135      140
66 cag ata agg aat gga cct cca gtc att cat tct gga atc aaa gac cta 480
67 Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
68 145      150      155      160
70 aaa gtc ttg aaa aca acc cag tct ggc ttt gaa gga ttc atc aag gac 528
71 Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
72      165      170      175
74 cag ttc acc acc ctc cct gag gtg aag gac cgg tgc ttt gcc acc caa 576
75 Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
76      180      185      190
78 gtg tac tgc aaa tgg cgc tac cac cag ggc aga gat gtg gac ttt gag 624
79 Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu
80      195      200      205
82 gcc acc tgg gac act gtt agg agc att gtc ctg cag aaa ttt gct ggg 672
83 Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly
84      210      215      220
86 ccc tat gac aaa ggc gag tac tca ccc tct gtg cag aag acc ctc tat 720
87 Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr
88 225      230      235      240
90 gat atc cag gtg ctc tcc ctg agc cga gtt cct gag ata gaa gat atg 768
91 Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met
92      245      250      255
94 gaa atc agc ctg cca aac att cac tac ttc aat ata gac atg tcc aaa 816
95 Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys
96      260      265      270
98 atg ggt ctg atc aac aag gaa gag gtc ttg ctg cca tta gac aat cca 864
99 Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro
100      275      280      285
102 tat gga aaa att act ggt aca gtc aag agg aag ttg tct tca aga ctg 912
103 Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu
104      290      295      300
106 tga 915
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113 <213> ORGANISM: Artificial Sequence
115 <220> FEATURE:
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122 Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln
123 20 25 30
125 Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
126 35 40 45
128 Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
129 50 55 60
131 Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys

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132 65          70          75          80
134 Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu
135          85          90          95
137 His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val
138          100          105          110
140 Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val
141          115          120          125
143 His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
144          130          135          140
146 Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
147 145          150          155          160
149 Lys Val Leu Lys Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
150          165          170          175
152 Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
153          180          185          190
155 Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu
156          195          200          205
158 Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly
159          210          215          220
161 Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr
162 225          230          235          240
164 Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met
165          245          250          255
167 Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys
168          260          265          270
170 Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro
171          275          280          285
173 Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu
174          290          295          300
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178 <211> LENGTH: 915
179 <212> TYPE: DNA
180 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:
183 <221> NAME/KEY: CDS
184 <222> LOCATION: (1)..(915)
186 <220> FEATURE:
187 <223> OTHER INFORMATION: Description of Artificial Sequence: pks chimera
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191 Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe
192 1 5 10 15
194 gtc cga act ggc tat ggg aag gat atg ata aaa gtt ctc cat att cag 96
195 Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln
196 20 25 30
198 cga gat gga aaa tat cac agc att aaa gag gtg gca act tca gtg caa 144
199 Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
200 35 40 45
202 ctg act ttg agc tcc aaa aaa gat tac ctg cat gga gac aat tca gat 192

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203	Leu	Thr	Leu	Ser	Ser	Lys	Lys	Asp	Tyr	Leu	His	Gly	Asp	Asn	Ser	Asp	
204		50					55					60					
206	gtc	atc	cct	aca	gac	acc	atc	aag	aac	aca	gtt	aat	gtc	ctg	gcg	aag	240
207	Val	Ile	Pro	Thr	Asp	Thr	Ile	Lys	Asn	Thr	Val	Asn	Val	Leu	Ala	Lys	
208	65					70					75				80		
210	ttc	aaa	ggc	atc	aaa	agc	ata	gaa	act	ttt	gct	gtg	act	atc	tgt	gag	288
211	Phe	Lys	Gly	Ile	Lys	Ser	Ile	Glu	Thr	Phe	Ala	Val	Thr	Ile	Cys	Glu	
212				85						90					95		
214	cat	ttc	ctt	tct	tcc	ttc	aag	cat	gtc	atc	aga	gct	caa	gtc	tat	gtg	336
215	His	Phe	Leu	Ser	Ser	Phe	Lys	His	Val	Ile	Arg	Ala	Gln	Val	Tyr	Val	
216				100					105					110			
218	gaa	gaa	gtt	cct	tgg	aag	cgt	ttt	gaa	aag	aat	gga	gtt	aag	cat	gtc	384
219	Glu	Glu	Val	Pro	Trp	Lys	Arg	Phe	Glu	Lys	Asn	Gly	Val	Lys	His	Val	
220			115				120						125				
222	cat	gca	ttt	att	tat	act	cct	act	gga	acg	cac	ttc	tgt	gag	gtt	gaa	432
223	His	Ala	Phe	Ile	Tyr	Thr	Pro	Thr	Gly	Thr	His	Phe	Cys	Glu	Val	Glu	
224		130				135					140						
226	cag	ata	agg	aat	gga	cct	cca	gtc	att	cat	tct	gga	atc	aaa	gac	cta	480
227	Gln	Ile	Arg	Asn	Gly	Pro	Pro	Val	Ile	His	Ser	Gly	Ile	Lys	Asp	Leu	
228	145				150					155					160		
230	aaa	gtc	ttg	aaa	aca	acc	cag	tct	ggc	ttt	gaa	gga	ttc	atc	aag	gac	528
231	Lys	Val	Leu	Lys	Thr	Thr	Gln	Ser	Gly	Phe	Glu	Gly	Phe	Ile	Lys	Asp	
232				165					170					175			
234	cag	ttc	acc	acc	ctc	cct	gag	gtg	aag	gac	cgg	tgc	ttt	gcc	acc	caa	576
235	Gln	Phe	Thr	Thr	Leu	Pro	Glu	Val	Lys	Asp	Arg	Cys	Phe	Ala	Thr	Gln	
236				180					185					190			
238	gtg	tac	tgc	aaa	tgg	cgc	tac	cac	cag	ggc	aga	gat	gtg	gac	ttt	gag	624
239	Val	Tyr	Cys	Lys	Trp	Arg	Tyr	His	Gln	Gly	Arg	Asp	Val	Asp	Phe	Glu	
240			195					200					205				
242	gcc	acc	tgg	gac	act	gtt	agg	agc	att	gtc	ctg	cag	aaa	ttt	gct	ggg	672
243	Ala	Thr	Trp	Asp	Thr	Val	Arg	Ser	Ile	Val	Leu	Gln	Lys	Phe	Ala	Gly	
244		210				215						220					
246	ccc	tat	gac	aaa	ggc	gag	tac	tcg	ccc	tct	gtc	cag	aag	aca	ctc	tat	720
247	Pro	Tyr	Asp	Lys	Gly	Glu	Tyr	Ser	Pro	Ser	Val	Gln	Lys	Thr	Leu	Tyr	
248	225				230						235				240		
250	gac	atc	cag	gtg	ctc	acc	ctg	ggc	cag	gtt	cct	gag	ata	gaa	gat	atg	768
251	Asp	Ile	Gln	Val	Leu	Thr	Leu	Gly	Gln	Val	Pro	Glu	Ile	Glu	Asp	Met	
252				245					250						255		
254	gaa	atc	agc	ctg	cca	aat	att	cac	tac	tta	aac	ata	gac	atg	tcc	aaa	816
255	Glu	Ile	Ser	Leu	Pro	Asn	Ile	His	Tyr	Leu	Asn	Ile	Asp	Met	Ser	Lys	
256			260						265					270			
258	atg	gga	ctg	atc	aac	aag	gaa	gag	gtc	ttg	cta	cct	tta	gac	aat	cca	864
259	Met	Gly	Leu	Ile	Asn	Lys	Glu	Glu	Val	Leu	Leu	Pro	Leu	Asp	Asn	Pro	
260			275					280					285				
262	tat	gga	aaa	att	act	ggt	aca	gtc	aag	agg	aag	ttg	tct	tca	aga	ctg	912
263	Tyr	Gly	Lys	Ile	Thr	Gly	Thr	Val	Lys	Arg	Lys	Leu	Ser	Ser	Arg	Leu	
264		290				295					300						
266	tga																915
270	<210> SEQ ID NO: 4																

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271 <211> LENGTH: 304
272 <212> TYPE: PRT
273 <213> ORGANISM: Artificial Sequence
275 <220> FEATURE:
276 <223> OTHER INFORMATION: Description of Artificial Sequence: pks chimera
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283           20           25           30
285 Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
286           35           40           45
288 Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
289           50           55           60
291 Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys
292   65           70           75           80
294 Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu
295           85           90           95
297 His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val
298           100          105          110
300 Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val
301           115          120          125
303 His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
304           130          135          140
306 Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
307  145          150          155          160
309 Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
310           165          170          175
312 Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
313           180          185          190
315 Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu
316           195          200          205
318 Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly
319           210          215          220
321 Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr
322  225          230          235          240
324 Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met
325           245          250          255
327 Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys
328           260          265          270
330 Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro
331           275          280          285
333 Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu
334           290          295          300
337 <210> SEQ ID NO: 5
338 <211> LENGTH: 304
339 <212> TYPE: PRT
340 <213> ORGANISM: Artificial Sequence
342 <220> FEATURE:

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/762,097A

DATE: 08/13/2002

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Input Set : A:\Seq LIST.txt

Output Set: N:\CRF3\08132002\I762097A.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date